GenCore vorsion 4 5 Copyright (c) 1993 - 2006 Compugen Ltd

OM protein - protein search, using sw model

Run on: April 24, 2002, 10:37:58; Search time 71.56 Seconds

(without alignments) 82.491 Million cell updates/sec

Fitle: US-09-525-998A-2_COPY_41_20]
Perfect score: 941
Sequence: 1 DSVCPGGKYTHPQNNSICCI......CSNCKKSLECTKICLPQIEN 161

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 1008 Maximum Match 1008 Listing lirst 45 summaries

Database : SwissProt_39:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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640 72 3 454 1 TNR1_MOUSF 095118 mus mus 674.5 71.7 471 1 TNR1_MOVIN 095118 mus mus 69 71.1 471 1 TNR1_MOVIN 095134 rattus 200.5 21.3 417 1 WSL1_HUMAN P669134 rattus 187.5 19.9 435 1 TNRC_HUMAN P66941 homo sa 187.5 19.9 435 1 TNRC_HUMAN P66941 homo sa 187.5 19.1 42.1 1 NURL_MOUSE 179.5 19.1 326 1 VT2_MYXYI P098138 homo sa 187.5 17.8 425 1 NURL_MOUSE 167.5 17.8 415 1 TNRC_MOUSE 167.5 17.8 416 1 TNRC_MOUSE 17.8 416 1 TNRC_MOUSE 17.8 416 mus mus 17.8 417 41 41.2 18.7 1 CN10 HOMAN 17.8 418 1	7	716.5	76.1	461		INK1 PIG	Sas
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ALIGNMENTS

-	INKI_HUMAN
<u> </u>	TNRT_HUMAN STANDARD; PRT; 455 AA, DIGATR
10	01-FEB-1991 (кел. 17, Created)
id.	01-FEB-1991 (ке). 17, Last sequence update)
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so	Homo sapiens (Human).
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3 3	Manimaria, Eucheria: Primates, Catafrillo, Rominidae: Home. Nebt Taxin-4606
Z X	
RP	SEQUENCE FROM N.A.
<u>2</u>	TISSUE-Flacenta;
	MEDLINE-90235285; PubMed 2158864;
	Schall Lie, Lewis M., Kollef Kiel, Loe A., Rice Giel, Word Sirik., Getanada (Grander C A Lentz R Paak H Roke M 1 Condool D
	"Molecular cloning and expression of a receptor for buman tumor
	necrosis lactor."
	Cell 61:361-370(1990).
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	"Molecular cloning and expression of the hyman 55 kd tumor necrosis
	Cell 61:351-359(1990).
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	Aderka D., Rollmann H., Wallach D.
	"Soluble forms of tumer actions factor teceptors (TAF As). The Min
=	for the type I TNF K, closed using aniles acid sequence data of its
	soluble forms encodes both the cell surface and a solutio form of t
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	EMBS 6. 313573 3276 1390). [4]
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	Himmiler A., Manner Fogy I., Brondke M., Schenzich E., Pffremmaler K.,
	Lantz M., Cleben I., Hauphmann R., Stratowa C., Adolt B.R.;
F.	"Melecular cluster and expendituous lamman and rat tumos necrosis
	factor receptor chain (p60) and its solutie derivative, number
 	necrosis factor-binding protein.":
<u>.</u>	DNA CCII Biol, 9:705-715(1990).
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XX	MEDITHE 91017509: EmbMed-2170974:
E.A.	Orac in the management of the contract of the
	CICLY I.M. D. Dodie C.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the BMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as bug as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH THEB
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"Two tumor necrosis Lactor-binding proteins puritied from human urine. Evidence for immunojaical cross reactivity with rell surface tumor necrosis factor receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93258809; PubMed-8387891; Bannor D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J., Bannor D.W., Detscher H., Lesslauer W. Broger C., Loetscher H., Lesslauer W. "Crystal structure of the soluble human 55 kd TNF receptor-human TNF beta complex: implications for TNF receptor activation.";
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DOMARY THE DOMAIN THAT INDUCES A SMASE IS FREGARLY IDENTICAL TO
THE DEATH DOMAIN. THE N. SMASE ACTIVATION DOMAIN (NSD) IS BOTH
NECESSARY AND SUFFICIENT FOR ACTIVATION OF N.-SMASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Naismith J.H., Devine T.O., Khono H., Sprang S.R.;
"Structures of the extraoglidar domain of the type I tumor mecrosis
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DATABASE: NAME-PROW: NOTE-CD quide CD120a entry:
WWW-"Hittp://www_urbi nim nih qocyptow/cd/ad120a him"
                                                                                                                                                                                                                                                Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P F; "Structure of the human TNF receptor I (p60) gene (TNFR1) and localization to chromosome 12pl3."; Genomics 13:219-224(1992).
expression of recombinant soluble TNF-binding protein.";
Proc. Natl. Acad. Sci. H.S.A. 87-7786-7784(1990)
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MEDLINE-97094982; Pubmed-8939750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 265:1531-1536(1990).
                                                                                                                                                                                              MFDLINE-92250049; PubMed 1315717;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprofein; Repeat; Signal; Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MISSING (IN REF. 4).
GPAA -> APP (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMOR NECROSIS FACTOR RECEPTOR 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 941; DB 1; Length 455; lint 0%; Pred, No. 5e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4CEFBA96D03B8225 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 KONTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPOTEN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEATH.
                                                                                                                                                                                                                                                                                                                                                                                                                  PPOSITE; PS50050; INFP_NGFR_2; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00652; TNFR_NGFR_1; 3.
PPOSITE: PS50050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50494 MW;
                                                                                                                                                                                                                                                                                                                PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                .TNFR_C6.
AL1511; CAA01558.1; -. A34899; GQHUT1.
                                                                                                                                                                                                                       interPro; IPR000488; Death.
                                                                                                                                                                                                                                                                                            PF00020; TNFR_C6; 4.
                                                                                                                                                                                                                                                                                                                                          SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor; Transmembrane;
                                                                                                                                                                                                                                                                     Pfam; PF00531; death; 1.
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143
158
1166
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                                                                                                                   1TNR; 31-JUL-94.
1NCF; 07-DEC-95.
1EXT; 11-JAN-97.
                                                A35010; A35010.
                                                                                                                                                                                                                                              IPR001368;
                                                                  $12057; $12057.
A38208; A38208.
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SIGNAL
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RESULT

M75864; AAA61201.1; JOINED. M75865; AAA61201.1; JOINED. M60275; AAA36756.1;

AAA36754.1; -...

M58286; M63121; M75866;

AAA61201.1; -

EMBL; X55313; CAA39021.1; ... EMBL; M33294: AAA04210 1: -

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COLOR DO SERVICION. RECEPTOR FOR THE ACTIVATED PEPERFORM. THE FERMILTIMS
COLOR DO SERVICION OF THE ACTIVATION WHICH THE FAND
CORREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
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                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Bel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TUMOR NECROSIS FACIOP PECEPTOR 1 PPPTURSOP (PE9) (TNP PI) (TNP-RI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NF-KAPPA B SIGNALING (BY SIMILARITY).

* SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

- SIMILARITY: CONTAINS I LANGER/YINETTYPE CYSTEINE-RICH REGION.

- SIMILARITY: CONTAINS I DEATH DOMAIN.
                                                                                                                                                                                       Sus scrota (Piq).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Cetartiodactyla; Suina; Suidae; Sus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE: PSSOU17; DEATH_DOMAIN; 1.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR NECROSIS FACTOR RECEIPTOR 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
  PRT; 461 AA
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TNFR-CYS 1.
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                                                                                                                                                                                                                                                                                                                                         TISSUE-Kidney;
MEDLINE-96011645; PubMed-7590278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00652: TNFR_NGFR_1: 3. PPOSITE: PS50050; TNFR_NGFR_2: ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; 1PR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probom; PD000771; TNFR_c6; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U19994; AAC48499.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 3.
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00208; TNFR; 3.
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SMART; SM00208; TNFR: 3
                                                                                                                                                                                                                                                                                                                                                                                         Suter B., Pauli U.H.;
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                                                                                                                                                                     INFRSF1A OR INFR1.
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    NCB1_Tax1D=9823;
TNR1_P1G
P50555;
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Eukaryota: Metagoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodwin R.G., Anderson D., Jerzy R., Haris L., Brannan C.L., Copeladd R.G., Anderson B., Dulth J.A., "Mcheclar Closins and expressions of the C.pe J and type 2 morine receptors for times and expressions are not the C.pe J and type 2 morine feceptors for times of the Cell. Riol. 11:8020-3026(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissumershis A.M.,
Gray P.W., Feldmann M., Foxwell B.M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       £2, 11.4, 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Clearing and expression of coNAs for two distinct murine tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.1%; Score 716.5; E8 1: Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nectoris factor respitors demonstrate one receptor is species specific.);
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Lewis M., Tartavlia L.A., Lee A., Rennett G.L., Rice G.C.,
Wong G.H., Chen E.Y., Goeddel D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acc. Matt. Acad. Sti. 7.3.A. 88.1830 1934(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.4%) Pred. No. 1.70-52;
tive 12, Mishat Acs 22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.1 POWING CORACT DISCREDING 1555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          50696 MW:
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Best Local Similarity 77.4%
Matches 120, Consentative
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SEQUENCE FROM N.A.
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ID TNRT_MOUSE
AC P25118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY)
SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF TNERL LEADS TO
                                                                                              "Molecular cloning and expression of the mouse Inf receptor type b_{\rm eff}; Immunogenetics 34:338-340(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, AFOLTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMOTRIMERIZATION, ONCE ACCREGATED THE RECEPTORS DEATH DOMAINS
PROVIDE A NOVEL MOLFOULAR INTERPACE THAI INTERACTS SPECIFICALLY
MITH THE DEATH DOMAIN OF FRAND, VARIOUS TRAND-INTERACTING
PROTEINS WITH AS TERES FIF AND POSSIFIED FACE, ARE RECEPTIFED TOWERS COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SHRYELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-PICH REGION.
-i- SIMILARITY: CONTAINS I DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: RECEPTOR FOR TWE ALPHA. THE ADAPTOR MOLECULE FADD
ECCEDITS CASPASE B TO THE ACTIVATED RECEPTOR. THE RESULTING
AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
PEPPORMS CASPASE BPOTED TITLE STRUKTION WHICH INITIATES THE
SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor: Transmembrane; Glycoptoin; Repeat; Signal; Apoptosis.
SIGNAL 1 Decembrane;
                                                                                                                                                                                                                                                                                                                                 wothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.; "Genomic organization and promoter function of the maxime tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POIENTIAL.
TUMOR NECROSIS FACTOR RECEPTOR 1.
                                                                                                                                                                           MEDLINE-94245292; PubMcd-8188324;
Robo H.E., Linthicum D.S.;
Nucleotide sequence of the INF type I receptor from a mouse
endothelioma cell line.";
                                                       MEDLINE-92039815; PubMed-1657766;
Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
                                                                                                                                                                                                                                                                                                                                                                        necrosis factor receptor beta gene.";
Mol. Emmunol, 30:165-175(1993).
                                                                                                                                                                                                                                                                                                                 MEDIJINE-93156721; PubMed-8381516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M76556; AAA40465.1; -...
EMBL; M88067; AAA40465.1; JOINED.
EMBL; M76655; AAA40465.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00652; TNFR_NGFR_1; 3. PROSITE: PS50050; TNFR_NGFR_2; 3. PROSITE: PS50017; DPATH_DOMAIN, 1
                                                                                                                                                                                                                                                         Immunogenetics 39:450-451(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
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MGD; MGI:1314884; Infrstla.
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Pfam; PF00020; TNFR_c6; 4.
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                    SEQUENCE FROM N.A.
                                         18SUE⊤Spleen;
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61 SCSKCPKEMGQVEISSCTVDRETVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 120
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                                                                                                                                                                                                                                 BY SIMILARITY.
N-LINKED (GICNAC. . .) (POTENTIAL).
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20-AUG-2001 (Rel. 40, Last annotation update)
TUMOR NECROSIS FACTOR PECEPTOR 1 PECURSOR (P60) (INF-R1) (INF-R1)
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Eskuryota, McLazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee B. K., Talyor M.J., Kehrli M.B.;
"Cloning of cDNA encoding bovine Lumor necrosis factor-receptor I
(TNF-RI).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RECEPTOR FOR TWE ALPHA. THE ADAPTOR MOLECULE FADD
RECKULTS CASIVASE 8 TO THE ACTIVATED RECEPTOR. THE RESULTING
AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
PERPOPMS CASPASE 8 PROTECTIVATE OF WHICH INITIALES THE
SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
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                                                                                                                                                                            N-SMASE ACTIVATION DOMAIN (NSD).
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71.3%; Pred. No. 1.7e·49;
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  EXTRACELLULAR (POTENTIAL)
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                                       CYTOPLASMIC (POTENTIAL).
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                                                                  4 X TNFR-CYS.
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                                                                                                                                INFR-CYS 3.
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20-AUG-2001 (Rel. 40, Last segu
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bicinformatics Estitute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib ch/announce;
or send an email to licensedisb-sib.ch).
              SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THERT LEADS TO HOMOTRIMERIZATION. ONCE AGGRECATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
                                                       WITH THE DEATH DOMAIN OF FRADD. VARIOUS TRADD-INTERACTING PROTEINS SIGH AS TRAFS, RIP AND POSSIBLY FALG, ARE FEVRUITED TO THER COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT EBASI TWO DISTINIL SIGNALING CASCADES, APOPTOSIS AND NE-KAPPA B SIGNALING (HY SIMILARITY).

1. SUBCHILLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

1. SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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71.6%; Pred. No. 5e-49;
Live 17; Mismatches 26; Indels 1; Gaps
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(GLGNAC. .) (POTENTIAL).
(GLGNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC) ) (PC
N-LINKED (GLCNAC) ) (PC
5243EF514DFE91C4 GRC64;
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 PROTEASES) MEDIATING APOPIOSIS (BY SIMILARITY)
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TNFR-CYS 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSTTE: PS00652; TNFR.MGFR_1; 3. PPOSTTE; PSS0050; TNFR.MGFR_2; 2. PROSTTE: PS50017; DMATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEATH
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151
51367 MW:
                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO01368; TNFR_c6
Pfam; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                EMBL: U90937: AAB65143.1;
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000488; Death.
                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00020; INFR_c6; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor, Transmembrane, SIGNAL 1
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SMART; SM00208; INFR; 3.
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151
471 AA;
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Best Local Similarity
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This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Himmler A., Maure-Foog, I., Kracuke M., Scheutien P., Filzenmaier K., Lantz M., olsson L., Hauptmann K., Stratowa C., Adolf G.K.;
"Molecular cloning and expression of human and rat tumor necrosis action to an analysis of human and rat tumor necrosis actor benefit chain (1605) and its soluble daridge tomor necrosis factor binding protein.";

DNA Cell Biol. 9:705-715(1990).

PROTEIN: REPERTA FOR THE ALPHA. THE MARTINE MOLECULE FABS
RECRUITS CASPASE 8 10 THE ACTIVATED RECEDOR, THE RESULING AGGREGATE CALLED THE DEATH-INDUTING SCOMPLEX (D187).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enkaryota, Metazoa, Chórdata, Craniata, Vertebrata, Bureleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Kattus
                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-ANR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
1006R NUCK-SIS FACION NECETION I PARCONSIN (FOU) (INFINI) (INFINI)
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SURGELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

- SIMILARITY: CHAPTAN A LA BEN'INFR-TYPE CYSTETNE-FICH REGION.

- SIMILARITY: CUNTAINS I DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PSOUGES: INFR_MSFR.1; 4.
PROSITE: PSSUUSO: INFR_MSFR.2; 4.
PROSITE: PSSUUT: DEALH_NOMAIN; 1.
RECEPTOT: Fransmembrane; Slycoprofein; Repeat: Slynal: Apoptosis.
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Pfam; PF00020; INFR_c6; 4.
ProDom; PD000771; INFR_c6; 1.
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InterPro; IPR000488; Death.
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      S: ANDARD;
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SMART; SM00208; INFR; 3.
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INK1_KAT
                                                                         P22934;
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
WSL-1 PROTEIN PRECURSOR (AFOFFORTS METAIIN: FEMERING DR3) (APOPTOSIS-MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)
(APOPTOSIS INDUCING PEMERING AIP) (AFO-3) (IYMPHG-YIE ASSECTATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T., Grinham C.J., Brown R., Farrow S.N.;
"A death domain containing receptor that mediates apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  STSKTRKEMGQVEISSTIVFFFTVHFFTVHFFNQPPRNJFGHFGHFWHSLHLIGHTSLHUTVHLSCQGE 120
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N.INKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSEL_BUMAN STANDARD; PRT; 417 AA.
Q93038; Q93036; Q93037; Q92048; P24845; Q904831; Q90722; P78507;
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                                                                                                       N-SMASE ACTIVATION DOMAIN (NSD).
                                                                                                                                                                                                                                                                                                                                                                    Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukoryola, Malazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                           43. Indels
EXTRACELLULAR (POTENTIAL).
                       CYTOPLASMIC (POLENTIAL),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KONIVCICHAGFFLRENEUVSCSNCKKSLECTKLCLPQIEN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.1%; Score 669; DB 1; 68.3%; Pred. No. 1.4e-48; attention 18. Mismalohos 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR OF DEATH) (LARD).
THERSF12 OR WSLI OR WSL OR AFOR OR DR3 OR DB83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 X TNFR-CYS.
                                                    INFR-CYS 1.
                                                               INFR-CYS 2.
INFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Umbilical vein endothelial cells;
                                                                                          TNFR-CYS 4
             POTENTIAL
                                                                                                                    DEATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLSSUE-Lymphoid;
MEDLINE-97088617; PubMed-8934525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                             50969 MW;
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                           461 AA;
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           TRANSMEM
DOMAIN
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chaudhary P.M., Hood L.E.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: INDUCES APOPTOSIS AND ACTIVATES NUCLEAR PACTOR KAPPA-B
-(NF-KAPPAB). DIRECTLY INTERACTS WITH TRADD ADAPTATOR MOLECULE. MAY
PLAY A ROLE IN REQUIATING LYMPHOCYPE HOMEOSTASIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER, INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
THE TWENT-ASSOCIATED MOLECULE TRAID AND THE TWRFT RECEIPOR TO
ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOFTOSIS AND
NF-KAPPA B SIGNALING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thome M., Bornand T., Hahne M., Schröeter M., Wilson A., French L.E., Browning J., Macdonald H.R., Tschopp J.; "TRAMP, a nevel appetus 8 mediating tenepter with segmence bomology to tumor necrosis tactor receptor 1 and Pas(Apo-1/CD95).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L., Goddard A.D., Hauer K.D., Ashkenazi A.; Appr.3, a new member of the tumor nectosis factor receptor tamily, contains a death domain and activates apoptosis and NF-Kappa-B."; Curr. Biol. 6:1669-1676(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLITIAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
ALTERNATIVE PRODUCTES: A ISOPOMENS; WEL-I/LARD-1A (SHOWN HERE),
WEL-SI/LARD-3 AND WEL-S2; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
                                                                                                                                                           Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "LARD, a new lymploid specific death domain containing receptor regulated by alternative pre mRNA splicing.", Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
MEDLINE-97081063; PubMed-8875942; Chinnalyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garq M., Duan D.P., Xing I., Gentz P., Ni J., Dixit V.M., "Signal transduction by DR3, a death domain-containing receptor related to TMFR-I and CD95."; Science 274:990-992(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R., MrMichael A.J., Bell J.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to licensewish sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain, and Fetal lung;
MEDLINE-97205335, FubMed-9052839;
                                                                                                                                                                                                                                                                 MEDLINE-97148200; PubMed-8994832;
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=9727273; PubMed=9114039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y09392; CAA70561.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U83600; AAB41435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMBL; Y09392; CAA70559.1; -. HMBL; Y09392; CAA70560.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE OF 4-417 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHOUFINCE OF 7-417 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U72763; AAC50819.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunity b:/9-88(1997).
                                                                                                                                           SEQUENCE FROM N.A. Degli-Esposti M.A.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                LISSUE-Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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VLGPGAPGWPCGPPPAWGHPDLHTPPLLASQAPGYCR (IN
                                                                                                                                                                                                                                                                                                                                                                              MFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
MEALTPPPATHLS -- SPWCAGNAFGFTGMCFGEGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                 L->A: SUPPRESSES HOMODIMERIZATION, TNFRI
INTERACTION, AND APPROSIS INDUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 GQVE.ISSOLVDKDIVGGCKKNQYRHYWSENLFQC----FNGSLGLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 HPQNNSICCTECHECHECTYLYNDCPGPGQDTDCRECESGSFTASENHIR-HCLSCSECPEEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.0 HEKTGLFFFPRACPAGHYLKAPGTEPGGNSTCLVGPGGTFLAWENHHNSEGARGGAGDEGA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNFRI INTERACTION.
D->A: SUPPRESSES HOMODIMERIZATION, AND
TNFRI INTERACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       L->A: SUPPRESSES HOMODIMERIZATION, AND
                                                                                                                                                                                                                                                                                                                                       STEGGCPFPGAAVGGWPQMPWQVELAGI VVFLLLGA
                                                                                                                                                                         Receptor; Apoptosis; Alternative splicing; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                    NHPTPTSCFQCSGSRCSWLALWSPSCLGPP (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 417,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72; Indels
                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN ISCHORM WSE-S1)
                                                                                                                                                                                                                                                                                                                                                                                                            ISOFORM WSL-S2).
MISSING (IN ISOFORM WSL-S2)
                                                                                                                                                                                                       WSL-1 PROTEIN.
EXIRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPR -> AAA (IN REF. 6).
P -> H (IN REF. 7).
P -> L (IN REF. 7).
A -> R (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R -> 1. (IN RBF. 1).
R -> H (IN RBF. 1).
F2263190P9446706_CRC64.
                                                                                                                                                                                                                            POLENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 EKQNTVCTCHAGFELRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.3%; Score 200.5; DB 1
29 8%; Pred No 5 8e-10;
                                                                                                                                                                                                                                                                                                                                                          ISPERM WSI-SI)
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                                                                                                                                                                                                                                                 4 X TNFR-CYS.
                                                                                                                                                                                                                                                                    TNFR-CYS 2.
INFR-CYS 3.
                                                                                                                                                                                                                                                            INFR-CYS 1
                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                              PROSITE: PS50017; DEATH_DOMAIN: 1.
                                                                                                                              Pfam; PF000z0; INFR_c6; 2.
PROSITE; PS00652; INFR_NGFR_1; 2.
U78029; AAB40918.1;
U44611; AAB3714.1;
U44504; AAC51309.1;
U44504; AAC51309.1;
U75381; AAC51192.1;
U75381; AAC51193.1;
U83597; AAB41432.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45385 MW;
                                                                                             InterPro: IPRO00488; Death.
InterPro: IPPO01368: PNFP_c6
                                                                                                                                                     PS50050; TNFR NGFR
                                                                                                                                                                                                                                                                                                                                                                   417
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417
199
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417
192
71
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                                                                                                                    Piam; PF00531; death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.1
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312
370
381
417 AA;
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Bost Local Similarity
                                                                          P19438; 1TNR.
                                                                                                                                                                                             356
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 EMBL; U78029;
                                                                                    MIM; 603366;
                                                                                                                                                                                                                DOMAIN
I RANSMEM
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CARBOHYD
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VARSPLIC
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CONFLICT
SEQUENCE
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SIGNAL
CHAIN
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                       EMBL
                                                                          HSSP;
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                                            MH.
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                                                                                                                                                                                                                                                                                                      MEDLINE-94225209; Pukmed-8171323;
Crowe P.D., van Arsdale T.L., Waller B.N., Ware C.F., Hession C.,
Ehrendels B., Eromanna J.L., Din W.S., Goodwin R.G., Smith C.A.;
Alementer a pupple of the specific receptor.";
Science 2.44:707-70(1994).
                       01-JUN-1954 (Rcl. 29, Created)
01-JUN-1954 (Rcl. 29, Last sequence update)
01-JUN-1954 (Rcl. 29, Last sequence update)
LIMBHOON (Rcl. 40, Last admostation update)
LIMBHOON BEILD RECEPTUR PRECUBERS (LUMOR NE) Resigned Receptur
2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR (TRESEPTOR))
                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR L/CATION: TYPE I MEMBRANE FROTEIN.
I SIMILARITY: CAMARINS A LA-MUER/INFR-INFR CYSTEINE RICH PEGION.
                                                                                                                                                                                                       MEDLINE-53252481; PubMod-8486360;
Baens M., Challanet M., Casalman J.J., den Beruhe H., Marynen P.,
Construction and evaluation of a factNA library of famou LZP
Lranscribed sequences derived from a samatto cell hybrid.";
Ocnomics 16:214-218(1993).
                                                                                                       Homo Sapiens (Human).
Enkaryota: Mviaroa: Chordata: Cramiata: Vertebrata: Enteleostomi;
Mammalia: Entheria: Primates: Catarrhini: Hominidae: Homo.
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YA SIMILAKITY.

N-LINKED (GLCNAV. ..) (POTENTIAL).

N-LINKEL (GLCNAV. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART: SM0208; INFR; 4.
PROSLIE; PS00652; INFR,NGFR_1; 2.
PROSLIE; PS50060; INFR_NGFR_2; 3.
Receptor: Transmembrane; Glycoprolein; Repeat: Slynal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYMPHOIGXIN-HEIA KECEPIOR
EXIRACELULAR (POIENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOFLASMIC (POTENTIAL)
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TNFR CYS 3.
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INFE_C6: 1.
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Probom; P0000771; INFR_c6:
                                                                                              LIBR OR INFOR OR INFRSE3.
STANDARD
                                                                                                                                                                                                                                                                                                                                                                                           IMMUNE DEVELOPMENT.
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1124
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1185
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                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                    NCBI_TaxID-9606;
                                                                                                                                                                                              18SUE=1.ive1;
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 TNRC_HUMAN
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REPEAT
DISULFID
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              P36941;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sebaul A., Patil N., Chao M.;
"A constitutive promoter directs expression of the nerve growth lactor receptor gene.";
                                                                                                                              49 EYYEPQHR FICCSECPPGIIVSAKC-SELEDIVOATCAENSYNEHWNYLTIQQLCEPCDP 106
                                                                                                                                                        68. PMOQVETSSOTIVTPRITVOGGRENÇERPWSENI FOGENGSI. - - CLAGIVAHLSGQE- - KQ. 122
                                                                                                                                                                         13; Caps
                                                                                                 8 KYTHPONNSTOTEKPHKSTYTZYNSPYGPODITIPČRKČESGSFTASENHIJRHCIJSCSKCRK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-87051725; PubMed-3022937;
Johnson D., Lanahan A., Hick C.P., Schgal A., Morgan C., Mercer E.,
                                                                                                                                                                                                                                                                                                                                                        01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Pel. 40, Last annotation update)
LOW-AFFINITY NERVE GROWIH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
(GPRO-LNOFR) (P75 ICD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBCELLULAR LACATION: TYPE I MEMBRANE PROTEIN.
-i- PTM. n- AND O-GLYCOSYLATED AND IS PHOSPHOKYLATED ON SERINE.
-i- SIMILARITY: CONTAINS A LA-MCFEKTINE-TYPE CYSTEINE-RICH REGION.
-i- SIMILARITY: CONTAINS I DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISHLFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (6) CELL, BIOL, B.3160-3167 (1988).
!- FUNCTION: LOW APPINITY RECEPTOR WHICH CAN BIND TO NGE, BONE, NT-3, AND NT-4.
                                         PR 1; Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteld
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                      71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bothwell M., Chao M.;
"Expression and structure of the buman NGF receptor";
Cell 47:545-554(1986).
46709 MW; 624626R6022R656F CRC64;
                                      19 9%; Score 187 %; FR 1
32.7%; Pred, No. 7.1e-09;
ive 17; Mismatches 71;
                                                                                                                                                                                                                                                                                                                       427 AA.
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                                                                                                                                                                                                                                PRT;
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MEDLINE-89096903; Pubmed-2850481;
                                                                                                                                                                                                                                                                                                                                               01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M14764; AAB59544.1; -. EMBL; M21621; AAA36363.1; -.
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InterPro; IPR001368; TNFR_C
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSF; P07174; INGR.
                                       query Match
Best Local Similarity
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135 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                       NGFR OR TNFRSF16
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SEQUENCE
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63 SKYPKEMYQVETSS-TTVDPPTVOGTPKNQYPHYWSENLFQCENCSLOLNGT-VHLSOQE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CPQCKYTHPQNNSTCCTKCHKGTYLYNDCPGPGODTDCREC-ESGSFTASENHLRHCLSC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 CPTGLYTH-- SGECCKACNLONGVAQPC-GANG TVCHPCLDSVTFSDVVSATFFCKPC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HINKEL (GLCNAC. . .) (POTENTIAL). B09FA143FB3D625B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91187885; PubMed-1849278; Lewis M., Tartrapla L.A., Lee A., Bennett G.L., Rice G.C., Mong G.H., Chen E.Y. 
"Cloning and expression of chNAs for two distinct murine tumor
                                                                                                                                          LOW-AFFINITY NERVE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 427;
                                                                             PROSITE; PS50017; DEATH_DOMAIN; 1.
Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1952 (Rel. 22, Last sequence update)
15-JUL 1999 (Rel. 38, Last annotation update)
TÜMÜR NEGRÖSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-E2) (P75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.4%; Score 182.5; DB 1 32.1%; Pred No. 1 Re 08;
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TNFR-CYS 3.
                                                                                                                                                                                                                                                                                    TNFR-CYS 4.
                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                          RECEPTOR.
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                                                                                                                                                                                                                                                                                                 DEATH.
                                            PROSITE; PS00652; INFR_NGFR_1; 3. PROSITE; PS50050; INFR_NGFR_2; 4.
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PS5113, P71893 3 1 22, Created)
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequ
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Pfam, PF00020, TNFR_c6, 4.
SMART; SM00005, DEATH; 1.
SMART; SM00208; TNFR; 3.
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                                                                                                              Phosphorylation; Signal
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427
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Best Local Similarity
Matches 52; Conserv
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                                                                                                      "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                             !- SIMILARITY: CONTAINS A LA NGEK/INFR-IYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUMOR NECROSIS FACTOR RECEPTOR 2.
necrosis factor receptors demonstrate one receptor is species
                                                             MEDLINE-91246168; PubMed 1645445,
Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.L.,
Copeland N.G., Jenkins N.A., Smith C.A.,
                                                                                                                                                                                                                                                        Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y., Submitted (MAY-1995) to the FWHI ChenRank/DERT databases -1- FUNCION: RECEPTOR FOR INF-ALPHA.
                                                                                                                                                                                        Jacob C.O., Liu J.;
Submitted (TAN-1996) to the EMBL/GenBack/PDRT databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
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                         Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
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PROSITE; PSSOOKA; TNPP_NGFP_2; 3.
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InterPrc: IPPO01969, INTP--6
Pfam; PF00020; INFR_C6; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: M60469; AAA39752.1; -. EMBL; M59378; AAA40463.1; -. EMBL; U39488; AAA85021.1; -. EMBL; X87128; CAA60618.1; ..
                                                                                                                                                                                                                                SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                             SEQUENCE OF 1-26 FROM N.A
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                                                    SECUENCE FROM N.A.
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Length 474,

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                                                                                                                                                                            63 SKORKIMOGVIISSOTVINITVOOOKKAGT 💛 NIITMAIRKITVITNOSIITAG TVIIS 117
                                                                                                                                                                                                                              99. SSCTTD: -QVETRACTKQQNRVCACEAGEYCALKTH: -S3S DRQCMRLSKCGPGFGVASS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Upton C., Macen J.L. Schreiber M., McFadden G.;
"Myxoma virus expresses a secreted protein with homology to the tumor
necrosis lactor receptor gene lamily that contributes to viral
                                                                            4 OPQORYTUPQONNSTOOTEVHROTETRYNFORMSTEEDERSESTETRASEMILLEDGE 6.2
                           14: Gaps
                                                                                                                           40 GQISQEYTORKAQMGCARCPROTVRHEGENKISDIVCADGEASMYLQVWNQFRICLSCS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virulence.";
Virology 184:370:382(1991).
-!- FUNCTION: BINDS TO INF ALPHA AND BILLA, PR-66ABLY PREVENTS INF TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chord-goxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REACH CELLULAR TARGET AND THERENY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE. SIMILARITY. CORKAINS A LA ROIK, THÈN TYPE CYSTELME NICH RESLOW.
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H LINKED (GL'NA'. ..) (F-TENTIAL).
H LINKED (GL'NA'. ..) (P-TENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) TUMOR NECROSIS FACTOR SCHULLE RECEPTOR DERCORSE (FROITH 12).
41.7%; Pred No. 2.5c 08;
17c 20, Mismatches 76; indeis
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INFR-CYS 2.
INFR-CYS 3.
INFR-CYS 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myxoma virus (strain Lausanne).
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EMBL: A23729, CAA01688.1,
PIR; A40566; GQVZML.
HSSP; P19438; TINE.
Hest Local Similarity 31,79 Matches 51, Conservative
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                                                                                                                                                                                                                                              Opton C., Delange A.M., McFadden G.; "Tunnerjannic poxylluses, genomic Organization and DNA sequence of the Lelomeric region of the Shope Libroma virus genome."; Virology 160:20-30(1987).
                                                                                                                                                                                   92 - ESQSCDKIRDRVCDCSAGNYCLLKGGEGERFCAPKIRCPAGYGVSGHIPPGDVL/TROP 150
                                                                                                                                                                                                                        93 RHYWSENLFOCENCSLCLNG-TVHLSCOEKONTVCTCHAGFFLRENECVSCSNCKKSLJC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           open reading trame from the Shope fibroma virus encodes a soluble
                                                                                           13 QUNSICTERCHROTYLYNDCPREQUATOPERECESGSFTASENHLRHCLSG-SKCRREMGQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem, Bicphys. Rcs. Commun. 176.335-342(1991).
-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses: dsDNA viruses, no PNA stage; Pexviridae, Chordopexvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91207415; PubMed-1850261;
Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
McFadden G., Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY, CONTAINS A LA NGFE/TNFR TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REACH CELLULAR TARGET AND THERENY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.
19.1%; Score 179.5; DB 1; Length 326; 27.4%; Pred. No. 2.6e.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR SOLURIE PECEPTOR PRECURSOR (PROTEIN T2)
                                       Indels
                                     67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 325 AA.
                                   19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shope fibroma virus (strain Kasza) (SFV).
                                                                                                                                                                                                                                                                                                                                                                                                                                 PPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M17433; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDI.INE-87321103; PubMcd-2820128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PS00652 INFP_NOFF_1, 2.
                                                                                                                                                72 VELSSCTVDRDTVCGCRKNQY - - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequ
15-JUE-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
Protom; PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the TNF receptor ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A23727; CAA01687.1;
                                   51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; B44692; B43692,
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCB1_Tax1D-10272;
                                                                                                                                                                                                                                                                                                  152 TKLCLP 157
                                                                                                                                                                                                                                                                                                                                 207 rp-cpp 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leporipoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP: P19438;
                                                                                                                                                                                                                                                                                                                                                                                                                               VI2_SFVKA
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION.
                     Lencal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                             VT2_SFVKA
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its solutent is in no way
modified and this statement is not removed. Usage by and lot commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 VELSSCTVDKDTVGGCKKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 - FSOFCURTHURVONCSIGNYCLLKGON-----GCKLCAPQI'----------KCFAG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APOPTOSIS, FAS-WEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).

-!- SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 QNNSTCCTKCHKGTYLYNDCPGPGQDTDCRECHSBSFTASENHLRHCLSC-SKCRKEMGQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 EKDÖLGCASCHPGEVASRLG-GPGSNTVCSPCEDGFFTASTNHAPACVSCROPCTGHLS- 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: PECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASE. THE ADAPTOR MOLECULE FADD RECRUITS CASEASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTECULTING CASPASE-8 ACTIVATION. ACTIVE CASPASE-8 INTILATES THE SUBSEQUENT CASCADE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bartling B , Hoffmann J , Holtz J , Schalz R , Heusch G , Parmer D.; Yagression of approxis associated genes in hibetrating and stunned monographism of an action of a contraction of a contracti
                                                                                                TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY CONTAINS A LA-NGFE/TNFF-TYPF CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUC-2001 (Rel. 40, Last annotation update)
45-JUL-101 (Rel. 40, Last annotation update)
(ARC-101 KELLIOK PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
TNFRSF6 OR APTI OR FAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazóa, Chordata, Cranjata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
8105.003.39198A71E CRC564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.9%; Score 178: DH 1; Length 325; 29.6%; Pred. No. 3.4e-08; Live 15, Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 AA.
                                                                                                                               4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 FELNENBURGVSGSMCKK . . . . . SUBCINIC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 YGVSGHTRAGPTLCEKCPPHTYSPSLSPTERC 164
                                                                                                                                                              TNFR-CYS 1.
                                                                                                                                                                                                TNFR-CYS 2.
                                                                                                                                                                                                                            TNFR-CYS 3.
TNFR-CYS 4.
PROSITE; PS50050; TNFR_NGFR_2; 1.
Receptor; Glycoprotein; Repeat; Signal.
                                                             POTENTIAL.
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                                                                                                                                                                                                                            147
186
                                                                                                                                                                                                                                                                                                                                                                                          238
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                                                                                                                                                                                                                                                                                                                                                                                                                         325 AA;
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                                                             SIGNAL
                                                                                                                               DOMA I N
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entities requires a librace agreement (See Attp.,/www.lsi wit objates and,) or send an email to licensewisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DSVCPQGKYIHPQNNSICCIKCHKGIYLYNNCPGFGQDIDGREGESG-SFTASENHLRHC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 PSERZPEGEH --- PFGGEGGGGGGGENZENGESPGGAPGGVPGSEGEDYTDKNHHSSKC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciuroquathi; Muridae; Muridae: Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Radeke M.J., Misko T.F., Bau C., Herzenberg L.A., Shooter E.M.; "Gene transfer and molecular cloning of the rat nerve growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metsis M., Himmusk T., Allikmets R., Saarma M., Persson H., "Regulatory elements and transcriptional regulation by testesterone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS50050; intramediate prosite; PS50017; DEAFH DOMAIN: 1. Apoptosis; Perceptor, Glycoprotein, Transmembrane, Repeat, Signal.
                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. ...) (POFENTIAL).
N-LINKED (GLCNAC. ...) (POFENTIAL).
5B8B036827558EIB GEGG4;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 18.8%; Score 176.5; DH 1; Length 332; Hest Local Similarity 29.1%; Pred. No. 4.7e·08;
                                                                                                                                                                                                                                                                                                                                                                                                           65; Indels
                                                                                                                                                                                             FASL RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 AA.
                                                                                                                                                                                                                                                   3 X TNFR-CYS.
INFR-CYS.1.
INFR-CYS.2.
INFR-CYS.3.
                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                       DEATH.
                                                                                      Pfam: PF00020; TNPR_C6; 3, SMART: SM0005; DEATH: 1. SMART: SM0005; TNFR; 3, SMART: SM00208; TNFR; 3, PROSITE; PS00652; TNFR_NGFR_2; 2, PROSITE; PS50050; TNFR_NGFR_2; 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-87115859; PubMed-3027580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93077038; PubMed-1446821;
                                      EMBL; AJ001202; CAA04596.1; ·.
                                                                                                                                                                                                                                                                                                                                              37592 MW
                                                  InterPro; IPR000488; Death.
InterPro; IPR001368; INFR_c6.
Pfam; PF00531; death; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 325:593-597(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegious (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GP80-LNGFR) (P75 1CD).
                                                                                                                                                                                                                                                                                                                                            332 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 EKÇNTVC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 PISNIKC 163
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193
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45
82
126
227
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                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGFR_RAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor.
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DOMAIN
REPEAT
REPEAT
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                                                                                               STRUCTURE BY NMR OF 334-418.
MEDLINE-97449145: PubMed-1955441;
Liepinsh E., Haq L.L., Otting G., Hanez C.E.,
"NMR Structure of the death domain of the p75 neurotrophin receptor.";
EMBO J. 16:4999-5005(1997).
       * the tat cerie growth factor receptor promoter.";
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-1- PIME N-AND TO CHOOSTALID AND TO CHOOSTHORYLAFID ON CHRINE.
-1- SIMILARITY: CHRIAINS A LA NOFR/THER TYPE CYSTEINE FIVE REGION.
-1- SIMILARITY: CONTAINS I DEATH DOMAIN.
                                                                                                                                                                                                                                                                             1. FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT 3. AND NT 4.
1. SUBSNIL: MSF RECEPTOR CAN FORM A REMODIMER IMPOUSH DISULFIDE BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOW APPINITY NERVE GROWTH PACTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peceptor, Neurospoesis, Iransmembrane, Olyooprotein, Repeat,
Phosphorylation, Sistan, 3D structure,
SIGNAL 1 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
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INFR-CYS 1.
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INFR CYS 3.
INFR CYS 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pram. PF00531; death; 1.

Plam. PF00020; TNFR_c6; 4.

SMART: SM00005; DEATH: 1.

PRAFT: SM00208; TNFR; 3.

PRAFT: SM00208; TNFR; 3.

PRAFT: P50055; INFR_NGFR_1; 3.

PRAFTE: P550050; INFR_NGFR_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X61265, NOT ANNOTATEL CHS. PIR. AZ6431; AZ6431, PDB, 1NGR, 29-JUL-97. InterPro: INRUGARR: Death. InterPro: INRUGARR: Death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.0
30.9%; 10.
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Bost Local Similarity 30.9
Matches 50, Conservative
sta 19115 is acted of the Gene 121:247-254(1992).
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                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rēl. 34, Last Sēguence update)
15-Jun.-1999 (Rel. 38, Last annotation update)
CD401. RECEPTOR PRECURSOR (R-CELL STREAGE ANTIGEN CD40) (RP50) (CDM40).
                                                                              63 SKOPKEMAQVEISS-OTVDPDTVOGOPKNQYPHYWSENLFQOFNOSLOLNGY-VHLSOQE 120
                                                                                                                 88 TEC----LGLQSMSAPCVEADDAVCRC---AYGYYQDEETGHGEAGSVCEVGSGLVFSQQD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generally structure and chromosomal mapping of the murine CD40 gene."; J. Lumunol, 149:3921-3926(1992).
                    4 CPQGKYTHPQNNSICCTKCHKGTYL/YNDCPGPGEGTECREC-ESGSFTASENHLRHCLSC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L, 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. 1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPF CYSTEINE-PICH PECTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enkarysta, Metazoa, Chordata, Cranjata, Verfebrata, Enteleostomi,
Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Musimae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "bilierential increase of an alternatively polyadenylated mRNA species of murine_C140 upon B lymphocyte activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BALBZC; TISSUB-Liver;
MEDLINE-93094586; PubMed-1281194;
Grimhldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SFP-1996) to the FMRL/ConRank/DDRL databases
                                                                                                                                                          121 KONTVC-TCHAGFFLRE----NECVSCSNCKKSLECTKLCLP 157
                                                                                                                                                                                               142 KONTVCEECPEGTYSDEANHVDPCLPCTVCEDTERQLRECTP 183
                                                                                                                                                                                                                                                                                                    289 AA.
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M83312; AAB08705.1; -.
EMBL: M94126; AAA37404.1; -.
M84129; AAA37404.1; -.
EMBL; M94128; AAA37404.1; JOINED.
EMBL; M94127; AAA37404.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92105763; PubMed-1370315;
TOFFOS R.M., Clark E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS00652; TNFR_NGFR_1; 1. PPOSITE: FSF0C59; TNFR_NGFE,2; 4.
                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunol. 148:620-626(1992).
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18SP, E25942 ICDF.

18SP, MGI 88446; Tolisi5.

InterPro; IPR001468; TNFR_c6.

"won0020; INFR_c6; 4.
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                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHOUENCE FROM N.A.
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Torres R.M.;
                                                                                                                                                                                                                                                                                                CD40_MQUSE
P27512.
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                                                                                                                                                                                                                                                        RESULT 14
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STRAIN-CYB: TISSUE-bung;
MEDLINE-66772804; PubMed-7594541;
Perror W P., Walter R.N., Hession C., Tizard R., Kozak C.A.,
Browning J.L., Ware C.F.;
"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
                                                                                                                                                                                                                                                                                                                                                                                                      64 KOPKEMOQVEISSCTVDRPDTVCGOPKNOYRIIYMSENLFQCFNCSLCLNG-TVIILSCQFKQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                      82 HCEFNQGLKVKKEGTAESDIVCTCKEGQ--HCISKBCEAGAGHTPCIPGFGVMEMATETT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-HETA, POSSIBLE FUNCTION IN
                                                                                                                                                                                                                                                                                                                                    4 CPOGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCKECESGSFTASENHLKHCLSCS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The murine lymphotoxin beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping."; Genomics 30:312-319(1995).
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                                                                                                                                                                                                                                                                                                                                                                   26 CSDKQYLH - - - DGQCCDLCQPGSRLJTSHCTAL - EKTOCHPCDSGEFSAQWNRETRCHQHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Verlebrata; Euteleostomi;
Mammalia; Eutheria, Rodentia; Sciuroquathi; Muridae; Musinae; Mus
                                                                                                                                                                                               .) (POTENTIAL)
Receptor: B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL 1 19 POTENTIAL.
                                                                                                                                                                                                                                                               17.8%; Score 167.5; DR 1; Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamura I., Tashiro K., Nazarca M., Nakano I., Sasayama S.,
                                                                                                                                                                                                                                                                                                 Indels
                                                    EXTRACELLUEAR (POTENTIAL).
                                                                                                                                                                                                            C791CB6D2FEA574E CRC64;
                                                                                     CYTOPLASMIC (POTENTIAL).
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-!- SUBCELLULAR LOCATION: TYPE | MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                               72;
                                                                                                                                                                                                                                                                                 Pred. No. 2.3e-07;
                                                                                                                                                                                             N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
LIMMHOTOXIN-HETA RECEPTOR PRECURSOR.
                                    CD401, RECEPTOR.
                                                                                                                                                                                                                                                                                                 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 NTVC-TCHAGFFIREN----ECVSCSNCK-KSLE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 DIVCHPCPVGFFSNOSSLFEKCYPWISCEDKNLE 173
                                                                                                         4 X INFR-CYS.
                                                                                                                        TNFR-CYS 1.
                                                                                                                                                          TNFR-CYS 3.
                                                                                                                                                                         TNFR-CYS 4.
                                                                                                                                          TNFR-CYS 2.
                                                                       POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rexpression. 7
Immunol. 155:5280-5288(1995).
                                                                                                                                                                                                             32111 MW;
                                                                                                                                                                                                                                                                                   29.98;
                                                                                                                                                                                                                                                                                                 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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193
215
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187
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                                                                                                                                                                                                            289 AA;
                                                                                                                                                                                                                                                                                   Best Local Similarity
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TRANSMEM
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                                                                                                                                     REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 KYTHPQNNSTGGTKCHKGTYLYNDGPGPGQDTDCKBCESGSFTASENHLRHCLSCSKCRK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIM
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                                                                                                                                                                                                                                                                                                                                                                             LYMPHOTOXIN-BETA RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                     Receptor: Transmembrane: Glycoprotein: Repeat; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
or send an email to licensedish-sib.ch).
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Job time: 672 sec
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InterPro; IPR001368; TNFR_c6.
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                                           EMBL; U29173; AAA68964.1;
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